

SEQUENCE LISTING

<110> CHATFIELD, STEVEN N.

<120> ATTENUATED BACTERIA USEFUL IN VACCINES

<130> 117-320

<140> US 09/646,925

<141>

<150> PCT/GB99/00935

<151> 1999-03-25

<150> GB 9806449.6

<151> 1998-03-25

<160> 28

<170> PatentIn Ver. 2.1

<210> 1

<211> 1690

<212> DNA

<213> Escherichia coli

<220>

<221> CDS

<222> (492)..(1562)

<400> 1

gtcgacgcgg tggatatctc tccagacgcg ctggcggttgc tgaacagaaa catcgaagaa 60
cacggctctga tccacaacgt cattccgatt cgttccgatc tgccgcga cttgccgaaa 120
gtgcagtacg acctgattgt cactaaccgg ccgtatgtcg atgcgaagat atgtccgacc 180
tgccaaacaa taccgccacg agccggaact gggctggca tctggcactg acggcctgaa 240
actgacgcgt cgcattctcg gtaacgcggc agattacctt gctgatgatg gcgtgttgc 300
ttgtgaagtc ggcaacagca tggtagatct tatggaacaa tatccggatg ttccgttcac 360
ctggctggag tttgataacg gcggcgatgg tgtgttatg ctcaccaaag agcagctt 420
tgccgcacga gaacatttcg cgattataa agattaagta aacacgcaaa cacaacaata 480
acggagccgt g atg gct gga aac aca att gga caa ctc ttt cgc gta acc 530
Met Ala Gly Asn Thr Ile Gly Gln Leu Phe Arg Val Thr
1 5 10
acc ttc ggc gaa tcg cac ggg ctg gcg ctc ggc tgc atc gtc gat ggt 578
Thr Phe Gly Glu Ser His Gly Leu Ala Leu Gly Cys Ile Val Asp Gly
15 20 25
gtt ccg cca ggc att ccg ctg acg gaa gcg gac ctg caa cat gac ctc 626
Val Pro Pro Gly Ile Pro Leu Thr Glu Ala Asp Leu Gln His Asp Leu

30	35	40	45	
gac cgt cgt cgc cct ggg aca tcg cgc tat acc acc cag cgc cgc gag Asp Arg Arg Arg Pro Gly Thr Ser Arg Tyr Thr Thr Gln Arg Arg Glu	50	55	60	674
ccg gat cag gtc aaa att ctc tcc ggt gtt ttt gaa ggc gtt act acc Pro Asp Gln Val Lys Ile Leu Ser Gly Val Phe Glu Gly Val Thr Thr	65	70	75	722
ggc acc agc att ggc ttg ttg atc gaa aac act gac cag cgc tct cag Gly Thr Ser Ile Gly Leu Leu Ile Glu Asn Thr Asp Gln Arg Ser Gln	80	85	90	770
gat tac agt gcg att aag gac gtt ttc cgt cca ggc cat gcc gat tac Asp Tyr Ser Ala Ile Lys Asp Val Phe Arg Pro Gly His Ala Asp Tyr	95	100	105	818
acc tac gaa caa aaa tac ggt ctg cgc gat tat cgc ggc ggt gga cgt Thr Tyr Glu Gln Lys Tyr Gly Leu Arg Asp Tyr Arg Gly Gly Arg	110	115	120	866
tct tcc gcc cgc gaa acc gcc atg cgc gtg gcg gca gga gct att gcc Ser Ser Ala Arg Glu Thr Ala Met Arg Val Ala Ala Gly Ala Ile Ala	130	135	140	914
aaa aaa tat ctc gcc gag aaa ttt ggt att gaa atc cgt ggc tgc ctg Lys Lys Tyr Leu Ala Glu Lys Phe Gly Ile Glu Ile Arg Gly Cys Leu	145	150	155	962
acc cag atg ggc gac att ccg ctg gat atc aaa gac tgg tcg cag gtc Thr Gln Met Gly Asp Ile Pro Leu Asp Ile Lys Asp Trp Ser Gln Val	160	165	170	1010
gag caa aat ccg ttt ttc tgc ccg gac ccc gac aaa atc gac gcg tta Glu Gln Asn Pro Phe Phe Cys Pro Asp Pro Asp Lys Ile Asp Ala Leu	175	180	185	1058
gac gag ttg atg cgt gcg ctg aaa aaa gag ggc gac tcc atc ggc gct Asp Glu Leu Met Arg Ala Leu Lys Glu Gly Asp Ser Ile Gly Ala	190	195	200	1106
aaa gtc acc gtt gtt gcc agt ggc gtt cct gcc gga ctt ggc gag ccg Lys Val Thr Val Val Ala Ser Gly Val Pro Ala Gly Leu Gly Pro	210	215	220	1154
gtc ttt gac cgc ctg gat gct gac atc gcc cat gcg ctg atg agc atc Val Phe Asp Arg Leu Asp Ala Asp Ile Ala His Ala Leu Met Ser Ile	225	230	235	1202
aac gcg gtg aaa ggc gtg gaa att ggc gac ggc ttt gac gtg gtg gcg Asn Ala Val Lys Gly Val Glu Ile Gly Asp Gly Phe Asp Val Val Ala	240	245	250	1250
ctg cgc ggc agc cag aac cgc gat gaa atc acc aaa gac ggt ttc cag Leu Arg Gly Ser Gln Asn Arg Asp Glu Ile Thr Lys Asp Gly Phe Gln	255	260	265	1298

agc aac cat gcg ggc ggc att ctc ggc ggt atc agc agc ggg cag caa Ser Asn His Ala Gly Gly Ile Leu Gly Gly Ile Ser Ser Gly Gln Gln	270	275	280	285	1346
atc att gcc cat atg gcg ctg aaa ccg acc tcc agc att acc gtg ccg Ile Ile Ala His Met Ala Leu Lys Pro Thr Ser Ser Ile Thr Val Pro	290		295	300	1394
ggt cgt acc att aac cgc ttt ggc gaa gaa gtt gag atg atc acc aaa Gly Arg Thr Ile Asn Arg Phe Gly Glu Glu Val Glu Met Ile Thr Lys	305		310	315	1442
ggc cgt cac gat ccc tgt gtc ggg atc cgc gca gtg ccg atc gca gaa Gly Arg His Asp Pro Cys Val Gly Ile Arg Ala Val Pro Ile Ala Glu	320		325	330	1490
gct gat ggc gat cgt ttt aat gga tca cct gtt acg gca acg ggc Ala Asn Ala Gly Asp Arg Phe Asn Gly Ser Pro Val Thr Ala Thr Gly	335		340	345	1538
gca aaa tgc cga tgt gaa gac tga tattccacgc tggtaaaaaa tgaataaaac Ala Lys Cys Arg Cys Glu Asp	350		355		1592
cgcgattgcg ctgctggctc tgcttgccag taggccagc ctggcagcga cgccgtggca aaaaataacc caacctgtgc cggtagcgc caaatcga					1652 1690

<210> 2
<211> 356
<212> PRT
<213> Escherichia coli

<400> 2 Met Ala Gly Asn Thr Ile Gly Gln Leu Phe Arg Val Thr Thr Phe Gly 1 5 10 15
Glu Ser His Gly Leu Ala Leu Gly Cys Ile Val Asp Gly Val Pro Pro 20 25 30
Gly Ile Pro Leu Thr Glu Ala Asp Leu Gln His Asp Leu Asp Arg Arg 35 40 45
Arg Pro Gly Thr Ser Arg Tyr Thr Thr Gln Arg Arg Glu Pro Asp Gln 50 55 60
Val Lys Ile Leu Ser Gly Val Phe Glu Gly Val Thr Thr Gly Thr Ser 65 70 75 80
Ile Gly Leu Leu Ile Glu Asn Thr Asp Gln Arg Ser Gln Asp Tyr Ser 85 90 95
Ala Ile Lys Asp Val Phe Arg Pro Gly His Ala Asp Tyr Thr Tyr Glu 100 105 110

Gln Lys Tyr Gly Leu Arg Asp Tyr Arg Gly Gly Gly Arg Ser Ser Ala
115 120 125

Arg Glu Thr Ala Met Arg Val Ala Ala Gly Ala Ile Ala Lys Lys Tyr
130 135 140

Leu Ala Glu Lys Phe Gly Ile Glu Ile Arg Gly Cys Leu Thr Gln Met
145 150 155 160

Gly Asp Ile Pro Leu Asp Ile Lys Asp Trp Ser Gln Val Glu Gln Asn
165 170 175

Pro Phe Phe Cys Pro Asp Pro Asp Lys Ile Asp Ala Leu Asp Glu Leu
180 185 190

Met Arg Ala Leu Lys Lys Glu Gly Asp Ser Ile Gly Ala Lys Val Thr
195 200 205

Val Val Ala Ser Gly Val Pro Ala Gly Leu Gly Glu Pro Val Phe Asp
210 215 220

Arg Leu Asp Ala Asp Ile Ala His Ala Leu Met Ser Ile Asn Ala Val
225 230 235 240

Lys Gly Val Glu Ile Gly Asp Gly Phe Asp Val Val Ala Leu Arg Gly
245 250 255

Ser Gln Asn Arg Asp Glu Ile Thr Lys Asp Gly Phe Gln Ser Asn His
260 265 270

Ala Gly Gly Ile Leu Gly Gly Ile Ser Ser Gly Gln Gln Ile Ile Ala
275 280 285

His Met Ala Leu Lys Pro Thr Ser Ser Ile Thr Val Pro Gly Arg Thr
290 295 300

Ile Asn Arg Phe Gly Glu Glu Val Glu Met Ile Thr Lys Gly Arg His
305 310 315 320

Asp Pro Cys Val Gly Ile Arg Ala Val Pro Ile Ala Glu Ala Asn Ala
325 330 335

Gly Asp Arg Phe Asn Gly Ser Pro Val Thr Ala Thr Gly Ala Lys Cys
340 345 350

Arg Cys Glu Asp
355

<210> 3
<211> 1713
<212> DNA
<213> Escherichia coli

<220>
<221> CDS
<222> (491)..(1594)

<400> 3
 gttacaaggc gttatagttt ttctgtggta gcacagaata atgaaaagtgc tgtaaagaag 60
 ggtaaaaaaaa accgaatgca aggcattccgg ttgaaatagg ggttaaacaga cattcagaaa 120
 tgaatgacgg taataaataa agttaatgtat gatagcggga gttattctag ttgcgagtga 180
 aggtttgtt ttgacattca gtgctgtcaa atacttaaga ataaggattt gatttttaacc 240
 ttgaattatt attgcttgat gtaggtgct tatttcgcca ttccgcaata atcttaaaaa 300
 gttcccttgc atttacattt tgaaacatct atagcgataa atgaaacatc taaaagttt 360
 tagtatcata ttcgtgttgg attattctgc atttttgggg agaatggact tgccgactga 420
 ttaatgaggg ttaatcagta tgcagtgca taaaaaagca aataaaggca tataacagag 480
 ggttaataac atg aaa gtt aaa gta ctg tcc ctc ctg gtc cca gct ctg 529
 Met Lys Val Lys Val Leu Ser Leu Leu Val Pro Ala Leu
 1 5 10
 ctg gta gca ggc gca gca aac gct gct gaa gtt tac aac aaa gac ggc 577
 Leu Val Ala Gly Ala Ala Asn Ala Ala Glu Val Tyr Asn Lys Asp Gly
 15 20 25
 aac aaa tta gat ctg tac ggt aaa gta gac ggc ctg cac tat ttc tct 625
 Asn Lys Leu Asp Leu Tyr Gly Lys Val Asp Gly Leu His Tyr Phe Ser
 30 35 40 45
 gac aac aaa gat gta gat ggc gac cag acc tac atg cgt ctt ggc ttc 673
 Asp Asn Lys Asp Val Asp Gly Asp Gln Thr Tyr Met Arg Leu Gly Phe
 50 55 60
 aaa ggt gaa act cag gtt act gac cag ctg acc ggt tac ggc cag tgg 721
 Lys Gly Glu Thr Gln Val Thr Asp Gln Leu Thr Gly Tyr Gly Gln Trp
 65 70 75
 gaa tat cag atc cag ggc aac agc gct gaa aac gaa aac aac tcc tgg 769
 Glu Tyr Gln Ile Gln Gly Asn Ser Ala Glu Asn Glu Asn Asn Ser Trp
 80 85 90
 acc cgt gtg gca ttc gca ggt ctg aaa ttc cag gat gtg ggt tct ttc 817
 Thr Arg Val Ala Phe Ala Gly Leu Lys Phe Gln Asp Val Gly Ser Phe
 95 100 105
 gac tac ggt cgt aac tac ggc gtt gtt tat gac gta act tcc tgg acc 865
 Asp Tyr Gly Arg Asn Tyr Gly Val Val Tyr Asp Val Thr Ser Trp Thr
 110 115 120 125
 gac gta ctg cca gaa ttc ggt ggt gac acc tac ggt tct gac aac ttc 913
 Asp Val Leu Pro Glu Phe Gly Gly Asp Thr Tyr Gly Ser Asp Asn Phe
 130 135 140
 atg cag cag cgt ggt aac ggc ttc gcg acc tac cgt aac act gac ttc 961
 Met Gln Gln Arg Gly Asn Gly Phe Ala Thr Tyr Arg Asn Thr Asp Phe
 145 150 155

ttc ggt ctg gtt gac ggc ctg aac ttt gct gtt cag tac cag ggt aaa Phe Gly Leu Val Asp Gly Leu Asn Phe Ala Val Gln Tyr Gln Gly Lys	160	165	170	1009
aac ggc aac cca tct ggt gaa ggc ttt act agt ggc gta act aac aac Asn Gly Asn Pro Ser Gly Glu Gly Phe Thr Ser Gly Val Thr Asn Asn	175	180	185	1057
ggt cgt gac gca ctg cgt caa aac ggc gac ggc gtc ggc ggt tct atc Gly Arg Asp Ala Leu Arg Gln Asn Gly Asp Gly Val Gly Ser Ile	190	195	200	205
act tat gat tac gaa ggt ttc ggt atc ggt ggt gcg atc tcc agc tcc Thr Tyr Asp Tyr Glu Gly Phe Gly Ile Gly Ala Ile Ser Ser Ser	210	215	220	1153
aaa cgt act gat gct cag aac acc gct gct tac atc ggt aac ggc gac Lys Arg Thr Asp Ala Gln Asn Thr Ala Ala Tyr Ile Gly Asn Gly Asp	225	230	235	1201
cgt gct gaa acc tac act ggt ggt ctg aaa tac gac gct aac aac atc Arg Ala Glu Thr Tyr Thr Gly Gly Leu Lys Tyr Asp Ala Asn Asn Ile	240	245	250	1249
tac ctg gct gct cag tac acc cag acc tac aac gca act cgc gta ggt Tyr Leu Ala Ala Gln Tyr Thr Gln Thr Tyr Asn Ala Thr Arg Val Gly	255	260	265	1297
tcc ctg ggt tgg gcg aac aaa gca cag aac ttc gaa gct gtt gct cag Ser Leu Gly Trp Ala Asn Lys Ala Gln Asn Phe Glu Ala Val Ala Gln	270	275	280	1345
tac cag ttc gac ttc ggt ctg cgt ccg tcc ctg gct tac ctg cag tct Tyr Gln Phe Asp Phe Gly Leu Arg Pro Ser Leu Ala Tyr Leu Gln Ser	290	295	300	1393
aaa ggt aaa aac ctg ggt cgt ggc tac gac gac gaa gat atc ctg aaa Lys Gly Lys Asn Leu Gly Arg Gly Tyr Asp Asp Glu Asp Ile Leu Lys	305	310	315	1441
tat gtt gat gtt ggt gct acc tac tac ttc aac aaa aac atg tcc acc Tyr Val Asp Val Gly Ala Thr Tyr Tyr Phe Asn Lys Asn Met Ser Thr	320	325	330	1489
tac gtt gac tac aaa atc aac ctg ctg gac gac aac cag ttc act cgt Tyr Val Asp Tyr Lys Ile Asn Leu Leu Asp Asp Asn Gln Phe Thr Arg	335	340	345	1537
gac gct ggc atc aac act gat aac atc gta gct ctg ggt ctg gtt tac Asp Ala Gly Ile Asn Thr Asp Asn Ile Val Ala Leu Gly Leu Val Tyr	350	355	360	1585
cag ttc taa tctcgattga tatcgaacaa gggcctgcgg gcccttttt Gln Phe				1634
cattgttttc agcgtacaaa ctcagtttt tggtgtactc ttgcgaccgt tcgcatgagg				1694

ataatcacgt acggaaata

<210> 4
<211> 367
<212> PRT
<213> Escherichia coli

<400> 4
Met Lys Val Lys Val Leu Ser Leu Leu Val Pro Ala Leu Leu Val Ala
1 5 10 15
Gly Ala Ala Asn Ala Ala Glu Val Tyr Asn Lys Asp Gly Asn Lys Leu
20 25 30
Asp Leu Tyr Gly Lys Val Asp Gly Leu His Tyr Phe Ser Asp Asn Lys
35 40 45
Asp Val Asp Gly Asp Gln Thr Tyr Met Arg Leu Gly Phe Lys Gly Glu
50 55 60
Thr Gln Val Thr Asp Gln Leu Thr Gly Tyr Gly Gln Trp Glu Tyr Gln
65 70 75 80
Ile Gln Gly Asn Ser Ala Glu Asn Glu Asn Ser Trp Thr Arg Val
85 90 95
Ala Phe Ala Gly Leu Lys Phe Gln Asp Val Gly Ser Phe Asp Tyr Gly
100 105 110
Arg Asn Tyr Gly Val Val Tyr Asp Val Thr Ser Trp Thr Asp Val Leu
115 120 125
Pro Glu Phe Gly Gly Asp Thr Tyr Gly Ser Asp Asn Phe Met Gln Gln
130 135 140
Arg Gly Asn Gly Phe Ala Thr Tyr Arg Asn Thr Asp Phe Phe Gly Leu
145 150 155 160
Val Asp Gly Leu Asn Phe Ala Val Gln Tyr Gln Gly Lys Asn Gly Asn
165 170 175
Pro Ser Gly Glu Gly Phe Thr Ser Gly Val Thr Asn Asn Gly Arg Asp
180 185 190
Ala Leu Arg Gln Asn Gly Asp Gly Val Gly Ser Ile Thr Tyr Asp
195 200 205
Tyr Glu Gly Phe Gly Ile Gly Gly Ala Ile Ser Ser Ser Lys Arg Thr
210 215 220
Asp Ala Gln Asn Thr Ala Ala Tyr Ile Gly Asn Gly Asp Arg Ala Glu
225 230 235 240
Thr Tyr Thr Gly Gly Leu Lys Tyr Asp Ala Asn Asn Ile Tyr Leu Ala
245 250 255

Ala Gln Tyr Thr Gln Thr Tyr Asn Ala Thr Arg Val Gly Ser Leu Gly
 260 265 270
 Trp Ala Asn Lys Ala Gln Asn Phe Glu Ala Val Ala Gln Tyr Gln Phe
 275 280 285
 Asp Phe Gly Leu Arg Pro Ser Leu Ala Tyr Leu Gln Ser Lys Gly Lys
 290 295 300
 Asn Leu Gly Arg Gly Tyr Asp Asp Glu Asp Ile Leu Lys Tyr Val Asp
 305 310 315 320
 Val Gly Ala Thr Tyr Tyr Phe Asn Lys Asn Met Ser Thr Tyr Val Asp
 325 330 335
 Tyr Lys Ile Asn Leu Leu Asp Asp Asn Gln Phe Thr Arg Asp Ala Gly
 340 345 350
 Ile Asn Thr Asp Asn Ile Val Ala Leu Gly Leu Val Tyr Gln Phe
 355 360 365

<210> 5
 <211> 1808
 <212> DNA
 <213> Escherichia coli

<220>
 <221> CDS
 <222> (457)..(1545)

<400> 5
 aaaactaatc cgcattctta ttgcggatta gtttttctt agctaatacg acaattttca 60
 tactatttt tggcattctg gatgtctgaa agaagatttt gtgccaggc gataaagttt 120
 ccatcagaaa caaaatttcc gtttagttaa tttaaatata aggaaatcat ataaatagat 180
 taaaattgct gtaaatatca tcacgtctct atggaaatat gacggtgttc acaaagttcc 240
 ttaaatttta ctttggtta catatttttt cttttgaaa ccaaatcttt atctttgttag 300
 cacttcacg gtagcgaaac gttagttga atggaaagat gcctgcagac acataaagac 360
 accaaaactct catcaatagt tccgtaaatt tttattgaca gaacttattg acggcagtgg 420
 caggtgtcat aaaaaaaacc atgagggtaa taaata atg atg aag cgc aat att 474
 Met Met Lys Arg Asn Ile
 1 5

ctg gca gtg atc gtc cct gct ctg tta gta gca ggt act gca aac gct 522
 Leu Ala Val Ile Val Pro Ala Leu Leu Val Ala Gly Thr Ala Asn Ala
 10 15 20

gca gaa atc tat aac aaa gat ggc aac aaa gta gat ctg tac ggt aaa 570
 Ala Glu Ile Tyr Asn Lys Asp Gly Asn Lys Val Asp Leu Tyr Gly Lys
 25 30 35

gct gtt ggt ctg cat tat ttt tcc aag ggt aac ggt gaa aac agt tac	618		
Ala Val Gly Leu His Tyr Phe Ser Lys Gly Asn Gly Glu Asn Ser Tyr			
40	45	50	
ggt ggc aat ggc gac atg acc tat gcc cgt ctt ggt ttt aaa ggg gaa	666		
Gly Gly Asn Gly Asp Met Thr Tyr Ala Arg Leu Gly Phe Lys Gly Glu			
55	60	65	70
act caa atc aat tcc gat ctg acc ggt tat ggt cag tgg gaa tat aac	714		
Thr Gln Ile Asn Ser Asp Leu Thr Gly Tyr Gly Gln Trp Glu Tyr Asn			
75	80	85	
ttc cag ggt aac aac tct gaa ggc gct gac gct caa act ggt aac aaa	762		
Phe Gln Gly Asn Asn Ser Glu Gly Ala Asp Ala Gln Thr Gly Asn Lys			
90	95	100	
acg cgt ctg gca ttc gcg ggt ctt aaa tac gct gac gtt ggt tct ttc	810		
Thr Arg Leu Ala Phe Ala Gly Leu Lys Tyr Ala Asp Val Gly Ser Phe			
105	110	115	
gat tac ggc cgt aac tac ggt gtg gtt tat gat gca ctg ggt tac acc	858		
Asp Tyr Gly Arg Asn Tyr Gly Val Val Tyr Asp Ala Leu Gly Tyr Thr			
120	125	130	
gat atg ctg cca gaa ttt ggt ggt gat act gca tac agc gat gac ttc	906		
Asp Met Leu Pro Glu Phe Gly Asp Thr Ala Tyr Ser Asp Asp Phe			
135	140	145	150
ttc gtt ggt cgt gtt ggc ggc gtt gct acc tat cgt aac tcc aac ttc	954		
Phe Val Gly Arg Val Gly Val Ala Thr Tyr Arg Asn Ser Asn Phe			
155	160	165	
ttt ggt ctg gtt gat ggc ctg aac ttc gct gtt cag tac ctg ggt aaa	1002		
Phe Gly Leu Val Asp Gly Leu Asn Phe Ala Val Gln Tyr Leu Gly Lys			
170	175	180	
aac gag cgt gac act gca cgc cgt tct aac ggc gac ggt gtt ggc ggt	1050		
Asn Glu Arg Asp Thr Ala Arg Arg Ser Asn Gly Asp Gly Val Gly Gly			
185	190	195	
tct atc agc tac gaa tac gaa ggc ttt ggt atc gtt ggt gct tat ggt	1098		
Ser Ile Ser Tyr Glu Tyr Gly Phe Gly Ile Val Gly Ala Tyr Gly			
200	205	210	
gca gct gac cgt acc aac ctg caa gaa gct caa cct ctt ggc aac ggt	1146		
Ala Ala Asp Arg Thr Asn Leu Gln Glu Ala Gln Pro Leu Gly Asn Gly			
215	220	225	230
aaa aaa gct gaa cag tgg gct act ggt ctg aag tac gac gcg aac aac	1194		
Lys Lys Ala Glu Gln Trp Ala Thr Gly Leu Lys Tyr Asp Ala Asn Asn			
235	240	245	
atc tac ctg gca gcg aac tac ggt gaa acc cgt aac gct acg ccg atc	1242		
Ile Tyr Leu Ala Ala Asn Tyr Gly Glu Thr Arg Asn Ala Thr Pro Ile			
250	255	260	

act aat aaa ttt aca aac acc agc ggc ttc gcc aac aaa acg caa gac Thr Asn Lys Phe Thr Asn Thr Ser Gly Phe Ala Asn Lys Thr Gln Asp	1290
265	270
275	
gtt ctg tta gtt gcg caa tac cag ttc gat ttc ggt ctg cgt ccg tcc Val Leu Leu Val Ala Gln Tyr Gln Phe Asp Phe Gly Leu Arg Pro Ser	1338
280	285
290	
atc gct tac acc aaa tct aaa gcg aaa gac gta gaa ggt atc ggt gat Ile Ala Tyr Thr Lys Ser Lys Ala Lys Asp Val Glu Gly Ile Gly Asp	1386
295	300
305	310
gtt gat ctg gtg aac tac ttt gaa gtg ggc gca acc tac tac ttc aac Val Asp Leu Val Asn Tyr Phe Glu Val Gly Ala Thr Tyr Tyr Phe Asn	1434
315	320
325	
aaa aac atg tcc acc tat gtt gac tac atc atc aac cag atc gat tct Lys Asn Met Ser Thr Tyr Val Asp Tyr Ile Ile Asn Gln Ile Asp Ser	1482
330	335
340	
gac aac aaa ctg ggc gta ggt tca gac gac acc gtt gct gtg ggt atc Asp Asn Lys Leu Gly Val Gly Ser Asp Asp Thr Val Ala Val Gly Ile	1530
345	350
355	
gtt tac cag ttc taa tagcacacct ctttgtaaaa tgccgaaaaa acaggactt Val Tyr Gln Phe	1585
360	
ggcctgttt ttttataacc ttccagagca atctcacgtc ttgcacaaac agcctgcgtt	1645
ttcatcagta atagttggaa tttgtaaat ctcccgttac cctgatagcg gacttccctt	1705
ctgtaaccat aatggAACCT cgtcatgttt gagaacatta ccggcgctcc tgccgACCCG	1765
attctgggcc tggccgatct gttcgtgcc gatgaacgtc ccg	1808

<210> 6
<211>362
<212> PRT
<213> Escherichia coli

Met Met Lys Arg Asn Ile Leu Ala Val Ile Val Pro Ala Leu Leu Val	
1	5
10	15
Ala Gly Thr Ala Asn Ala Ala Glu Ile Tyr Asn Lys Asp Gly Asn Lys	
20	25
30	
Val Asp Leu Tyr Gly Lys Ala Val Gly Leu His Tyr Phe Ser Lys Gly	
35	40
45	
Asn Gly Glu Asn Ser Tyr Gly Gly Asn Gly Asp Met Thr Tyr Ala Arg	
50	55
60	
Leu Gly Phe Lys Gly Glu Thr Gln Ile Asn Ser Asp Leu Thr Gly Tyr	
65	70
75	
80	

Gly Gln Trp Glu Tyr Asn Phe Gln Gly Asn Asn Ser Glu Gly Ala Asp
85 90 95

Ala Gln Thr Gly Asn Lys Thr Arg Leu Ala Phe Ala Gly Leu Lys Tyr
100 105 110

Ala Asp Val Gly Ser Phe Asp Tyr Gly Arg Asn Tyr Gly Val Val Tyr
115 120 125

Asp Ala Leu Gly Tyr Thr Asp Met Leu Pro Glu Phe Gly Gly Asp Thr
130 135 140

Ala Tyr Ser Asp Asp Phe Phe Val Gly Arg Val Gly Gly Val Ala Thr
145 150 155 160

Tyr Arg Asn Ser Asn Phe Phe Gly Leu Val Asp Gly Leu Asn Phe Ala
165 170 175

Val Gln Tyr Leu Gly Lys Asn Glu Arg Asp Thr Ala Arg Arg Ser Asn
180 185 190

Gly Asp Gly Val Gly Ser Ile Ser Tyr Glu Tyr Glu Gly Phe Gly
195 200 205

Ile Val Gly Ala Tyr Gly Ala Ala Asp Arg Thr Asn Leu Gln Glu Ala
210 215 220

Gln Pro Leu Gly Asn Gly Lys Lys Ala Glu Gln Trp Ala Thr Gly Leu
225 230 235 240

Lys Tyr Asp Ala Asn Asn Ile Tyr Leu Ala Ala Asn Tyr Gly Glu Thr
245 250 255

Arg Asn Ala Thr Pro Ile Thr Asn Lys Phe Thr Asn Thr Ser Gly Phe
260 265 270

Ala Asn Lys Thr Gln Asp Val Leu Leu Val Ala Gln Tyr Gln Phe Asp
275 280 285

Phe Gly Leu Arg Pro Ser Ile Ala Tyr Thr Lys Ser Lys Ala Lys Asp
290 295 300

Val Glu Gly Ile Gly Asp Val Asp Leu Val Asn Tyr Phe Glu Val Gly
305 310 315 320

Ala Thr Tyr Tyr Phe Asn Lys Asn Met Ser Thr Tyr Val Asp Tyr Ile
325 330 335

Ile Asn Gln Ile Asp Ser Asp Asn Lys Leu Gly Val Gly Ser Asp Asp
340 345 350

Thr Val Ala Val Gly Ile Val Tyr Gln Phe
355 360

<210> 7
<211> 35

<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PCR primer

<400> 7
atctgtttgt tgagctcagc aatctatttg caacc 35

<210> 8
<211> 34
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:PCR primer

<400> 8
ttttttgcca gcatgccggc agccacgcgt agtg 34

<210> 9
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:PCR primer

<400> 9
ctcgaggctt agctctattt attaccctca tgg 33

<210> 10
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:PCR primer

<400> 10
gagctaagcc tcgagtaata gcacacctct ttg 33

<210> 11
<211> 34
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:PCR primer

<400> 11
ttgctggaaa gtcgacggat gttaattatt tgtg 34

<210> 12
<211> 35
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:PCR primer

<400> 12 35
ggccaaagcc gagctcattc accagcggcc cgacg

<210> 13
<211> 32
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:PCR primer

<400> 13 32
gctaaggcctc gagtaatctc gattgatatac cg

<210> 14
<211> 31
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:PCR primer

<400> 14 31
ctcgaggctt agcggttatta accctctgtt a

<210> 15
<211> 34
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:PCR primer

<400> 15 34
ccgcgcgtcg tcttagagtga actgatcaac aata

<210> 16
<211> 34
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:PCR primer

<400> 16 34
atgcgcgca gagctcaacc agcgtcgac tttg

<210> 17
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:PCR primer

<400> 17 30
ctcgaggcat gctgaataaa accgcgattg

<210> 18
<211> 31
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:PCR primer

<400> 18 31
gcatgccctc gagggctccg ttattgttgt g

<210> 19
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:PCR primer

<400> 19 25
tgattccctt tgttgcgaag gcgaa

<210> 20
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:PCR primer

<400> 20 25
attaagatac ccaagtaata ctcaa

<210> 21
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:PCR primer

<400> 21 20
gctttaaag gatccttagtt

<210> 22
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:PCR primer

<400> 22 20
ggtatcttt ccggattgtc

<210> 23
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:PCR primer

<400> 23 22
catgttccgg aggttaatatg aa

<210> 24
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:PCR primer

<400> 24 22
agttcccttt atattattaa ta

<210> 25
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:PCR primer

<400> 25 20
tggagtttat atgaaaactaa

<210> 26
<211> 20
<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:PCR primer

<400> 26 20
tgacttagtc aggataattg

<210> 27

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:PCR primer

<400> 27 20
atacttatta ataggtcttt

<210> 28

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:PCR primer

<400> 28 20
ttgtcgaagt aattgttata